

\*\*\*\*\* Welcome to STN International \*\*\*\*\*

NEWS 1 Web Page URLs for STN Seminar Schedule - N. America

NEWS 2 "Ask CAS" for self-help around the clock

NEWS 3 JAN 27 Source of Registration (SR) information in REGISTRY updated and searchable

NEWS 4 JAN 27 A new search aid, the Company Name Thesaurus, available in CA/Caplus

NEWS 5 FEB 05 German (DE) application and patent publication number format changes

NEWS 6 MAR 03 MEDLINE and LMEEDLINE reloaded

NEWS 7 MAR 03 MEDLINE file segment of TOXCENTER reloaded

NEWS 8 MAR 03 FRANCESAT now available on STN

NEWS 9 MAR 29 Pharmaceutical Substances (PS) now available on STN

NEWS 10 MAR 29 WIFW now available on STN

NEWS 11 MAR 29 New monthly current-awareness alert (SDI) frequency in RAPRA

NEWS 12 APR 26 PROMT: New display field available

NEWS 13 APR 26 IFIPAT/IFIUDB/IFICDB: New super search and display field available

NEWS 14 APR 26 LITLERT now available on STN

NEWS 15 APR 27 NLDB: New search and display fields available

NEWS 16 May 10 PROUSDR: One FREE connect hour, per account, in both May and June 2004

NEWS 18 May 12 EXTEND option available in structure searching

NEWS 19 May 12 Polymer links for the POLYLINK command completed in REGISTRY

NEWS 20 May 17 PRFULL now available on STN

NEWS 21 May 27 STN User Update to be held June 7 and June 8 at the SLA 2004 Conference

NEWS 22 May 27 New UPM (Update Code Maximum) field for more efficient patent SDIs in Caplus

NEWS 23 May 27 Caplus super roles and document types searchable in REGISTRY

NEWS 24 May 27 Explore APOLLIT with free connect time in June 2004

NEWS EXPRESS MARCH 31 CURRENT WINDOWS VERSION IS V7.00A. CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP).

STN Operating Hours Plus Help Desk Availability

General Internet Information

Welcome Banner and News Items

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CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that specific topic.

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\*\*\*\*\* STN Columbus \*\*\*\*\*

FILE 'HOME' ENTERED AT 20:39:06 ON 08 JUN 2004

=> index biosci

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE ENTRY 0.21

TOTAL SESSION 0.21

FULL ESTIMATED COST

INDEX 'ADISCTI', ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOSUBSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCELLIT, CAPLUS, CEABA-VTE, CEN, CIN, CONFSCI, CROPE, CROPU, DISSABS, DDFB, DDFU, DGENE, DRUGB, DRUGMONOG2, ...' ENTERED AT 20:39:16 ON 08 JUN 2004

70 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view search error messages that display as 0\* with SET DETAIL OFF.

=> s (thermogenic (w) protein) (p) (skunk (w) cabbage)

0\* FILE ADISNEWS  
0\* FILE BIOCOMMERCE  
0\* FILE BIOTECHABS  
0\* FILE BIOTECHDS  
0\* FILE BIOTECHNO  
0\* FILE CEABA-VTE  
0\* FILE CIN

25 FILES SEARCHED...

0\* FILE ESIORBASE  
0\* FILE FEDRIP  
0\* FILE FOMAD  
0\* FILE FOREGE  
0\* FILE FROSTI  
0\* FILE FSTA  
1 FILE IFIPAT  
0\* FILE KOSMET  
0\* FILE MEDICONF  
0\* FILE NTIS  
0\* FILE NUTRACEUT  
0\* FILE PASCAL  
0\* FILE PHARMAML

62 FILES SEARCHED...

1 FILES HAVE ONE OR MORE ANSWERS, 70 FILES SEARCHED IN STNINDEX

L1 QUE (THERMOGENIC (W) PROTEIN) (P) (SKUNK (W) CABBAGE)

=> file hits

COST IN U.S. DOLLARS

SINCE FILE ENTRY 1.14

TOTAL SESSION 1.35

FULL ESTIMATED COST

FILE 'IFIPAT' ENTERED AT 20:40:37 ON 08 JUN 2004

COPYRIGHT (C) 2004 IFI CLAIMS(R) Patent Services (IFI)

FILE COVERS 1950 TO PATENT PUBLICATION DATE: 3 JUN 2004 (20040603/PD)

FILE LAST UPDATED: 4 JUN 2004 (20040604/ED)

HIGHEST GRANTED PATENT NUMBER: US2004087609

HIGHEST APPLICATION PUBLICATION NUMBER: US2004107471

UNITERM INDEXING IS AVAILABLE IN THE IFIUDB FILE

UNITERM INDEXING LAST UPDATED: 27 MAY 2004 (20040527/UP)

INDEXING CURRENT THROUGH PAT PUB DATE: 25 Nov 2003 (20031125/PD)  
IFIPAT has been relocated (12/21/2003). See HELP RLOAD for details.

=> s 11

64 THERMOGENIC  
65668 PROTEIN  
37 SKUNK  
450 CABBAGE  
L2 1 (THERMOGENIC (W) PROTEIN) (P) (SKUNK (W) CABBAGE)  
=> d 12 bib ab

L2 ANSWER 1 OF 1 IFIPAT COPYRIGHT 2004 IFI on STN  
AN 10560887 IFIPAT:IFIUB:IFICDB  
TI PLANT THERMOGENIC GENES AND PROTEINS  
INF Ito, Kikukatsu, Iwate, JP  
IN Ito Kikukatsu (JP)  
PAF Unassigned  
PA Unassigned Or Assigned To Individual (68000)  
AG WASHINGTON, LIND & PONACK, L.L.P., 2033 K STREET N. W., SUITE 800,  
WASHINGTON, DC, 20006-1021, US  
PI US 2004068105 A1 20040408  
RI US 2003-671628 20030929  
RLI WO 2000-JP3806 20000612 Section 371 PCT Filing UNKNOWN  
US 2002-9962 20020123 DIVISION  
PRAI JP 1999-167439 19990614  
FI US 2004068105 20040408  
DT Utility: Patent Application - First Publication  
FS CHEMICAL  
APPLICATION  
CLMN 6  
GI 8 Figure(s).

FIG. 1 shows the change of the temperature of the spadix in skunk cabbage and that of ambient temperature with a lapse of time.  
FIG. 2 shows the results of northern blotting, indicating the expression profile of SfUCPa (A) and SfUCPb (B) in the spadix and leaf of skunk cabbage at room temperature (RI) and during cold treatment (4 degrees C. for 3 days). The lower figures respectively show the results of etidium bromide staining of non-decomposed rRNA.  
FIG. 3 compares the alignment of amino acid sequences of SfUCPa and SfUCPb, together with potato UCP (StUCP), Arabidopsis UCP (AtPUMP) and human UCP. The asterisk (\*) attached under the sequences indicate the same amino acid sequence, and the dot (.) indicates the conservative change in all of the sequences. The boldface indicates the same sequence between SfUCPa and SfUCPb. The gap introduced to optimize the sequence alignment is indicated by a dash (-). The alignment was made using a CLUSTAL W program. The characteristic domains of energy transfer proteins (I-VI) above the upper sequence show estimated transmembrane domains.  
FIG. 4 shows a hydrophobic plot of SfUCPa. The vertical axis indicates the degree of hydrophobicity and the estimated transmembrane domains are indicated by TM1 to TM6.  
FIG. 5 shows a diagrammatic illustration of SfUCPa topology in the mitochondria membrane.  
FIG. 6 shows a hydrophobic plot of SfUCPb. The vertical axis indicates the degree of hydrophobicity and the estimated transmembrane domains are

indicated by TM1 to TM4 and TM6.  
FIG. 7 shows a diagrammatic illustration of SfUCPb topology in the mitochondria membrane.  
FIG. 8 shows the results of in vitro translation using respective cDNAs of the genes SfUCPa and SfUCPb as templates. ( ) indicates a control, S a sense RNA, and AS an antisense RNA. The asterisk (\*) indicates a non-specific product and the empty circle denotes the position of a low molecular translated artificial product synthesized from a small ORF. Th inventions of his application include thermogenic genes named SfUCPa and SfUCPb which are derived from skunk cabbage. cDNA of each gene comprises the base sequence of SEQ ID NO: 1 and 3, respectively. Thermogenic proteins, SfUCPa and SfUCPb, are expressed from genes SfUCPa and SfUCPb, comprises the amino acid sequence of SEQ ID NO: 2 and 4.

=> d his

(FILE 'HOME' ENTERED AT 20:39:06 ON 08 JUN 2004)

INDEX 'ADISCTI', ADISINISIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPU, DISSASS, DDFB, DDFU, DGENE, DRUGB, DRUGMONOG2, ...' ENTERED AT 20:39:16 ON 08 JUN 2004

SEA (THERMOGENIC (W) PROTEIN) (P) (SKUNK (W) CABBAGE)

0\* FILE ADISNEWS  
0\* FILE BIOCOMMERCE  
0\* FILE BIOTECHABS  
0\* FILE BIOTECHDS  
0\* FILE BIOTECHNO  
0\* FILE CEABA-VTB  
0\* FILE CIN  
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0\* FILE FEDRIP  
0\* FILE FOWAD  
0\* FILE FOREGE  
0\* FILE FROSTI  
0\* FILE FSTA  
1 FILE IFIPAT  
0 FILE KOSMET  
0 FILE MEDICONF  
0 FILE NTIS  
0 FILE NUTRACEUT  
0 FILE PASCAL  
0\* FILE PHARMAML  
QUE (THERMOGENIC (W) PROTEIN) (P) (SKUNK (W) CABBAGE)

L1

FILE 'IFIPAT' ENTERED AT 20:40:37 ON 08 JUN 2004

L2 1 S LI

=> log y

COST IN U.S. DOLLARS SINCE FILE TOTAL  
FULL ESTIMATED COST ENTRY SESSION  
5.91 7.26

STN INTERNATIONAL LOGOFF AT 20:40:57 ON 08 JUN 2004

OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 16:59:57 ; Search time 588.22 Seconds

Title: US-10-671-628-1  
(without alignment)  
Perfect score: 1525  
Sequence: 11282.980 Million cell updates/sec

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

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11: gb.scs.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

15: em.ba.\*

16: em.fun.\*

17: em.hum.\*

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27: em.sts.\*

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32: em.htg\_other.\*  
33: em.htg\_mus.\*  
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38: em\_sy.\*  
39: em.htgo\_hum.\*  
40: em.htgo\_mus.\*  
41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1525	100.0	1525	6	ES0743	ES0743 Plant exoth
2	1525	100.0	1525	6	BD011855	BD011855 Thermogen
3	1525	100.0	1525	8	AB024733	AB024733 Symplocar
4	1076.6	70.6	2991	6	ES0744	ES0744 Plant exoth
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7	646.4	42.4	1209	8	AB088762	AB088762 Helicodic
8	537	35.2	1434	8	AF472619	AF472619 Lycopersi
9	537	35.2	1434	8	STUCPMRNA	Y11220 Solanum tub
10	502.4	32.9	1240	8	ATMTUNCOU	AJ001264 Arabidops
11	500.8	32.8	920	6	AX651736	AX651736 Sequence
12	500.8	32.8	921	6	AX506066	AX506066 Sequence
13	500.8	32.8	921	8	AF146226	AF146226 Arabidops
14	500.8	32.8	952	8	AY091185	AY091185 Arabidops
15	500.8	32.8	1225	6	AX269361	AX269361 Sequence
16	500.8	32.8	1225	8	ATPUMP	AJ223983 Arabidops
17	500.8	32.8	1274	8	AY056272	AY056272 Arabidops
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21	471.4	30.9	1227	8	AY088200	AY088200 Arabidops
22	443.2	29.1	1263	8	AK061318	AK061318 Oryza sat
23	441.6	29.0	1179	8	AK104090	AK104090 Oryza sat
24	437.2	28.7	1243	8	AF461732	AF461732 Zea mays
25	422.2	27.7	915	6	AX653777	AX653777 Sequence
26	415.4	27.2	974	6	AX269364	AX269364 Sequence
27	415.4	27.2	974	8	AB042428	AB042428 Triticum
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35	176.6	11.6	1483	5	BC056737	BC056737 Danio rer
36	174	11.4	1698	5	BC053173	BC053173 Danio rer



COMMENT

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RESULT 2	
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LOCUS	
DEFINITION	Thermogenesis genes and thermogenesis proteins in plant.
ACCESSION	BD011855
VERSION	BD011855.1 GI:22092044
KEYWORDS	WO 0077211-A/1.
ORGANISM	Symplocarpus foetidus Symplocarpus foetidus Symplocarctae; Viridiplantae Eukaryota; Viridiphyta; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Symplocarpus. 1 (bases 1 to 1525)
REFERENCE	Ito,K.
AUTHORS	
TITLE	Thermogenesis genes and thermogenesis proteins in plant
JOURNAL	Patent: WO 0077211-A 1 21-DEC-2000;

JAPAN SCIENCE AND TECHNOLOGY CORP, KIKUKATSU ITO	
OS	Symplocarpus foetidus
PN	WO 0077211-A/1
PD	21-DEC-2000
PF	12-JUN-2000 WO 2000JP03806
PR	14-JUN-1999 JP 99P 167439
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PC	C12N15/29,C07K14/415
CC	
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DB	241 TCTACTTGGGAGCCCATTTGATCGAGGTTTTCCGGCGAGATGGGCGCATCAGGCCCGAGG 300
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DB	361 TGCACGATTCGTTGGGACATGCTTAAGTTAGGCTTCACTCCCAAAAGAAACGAGTAACA 420
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Db 1501 TTTTAAAAAAGAAAAAAGAAAA 1525

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DEFINITION  
ACCESSION AB024733  
VERSION AB024733.1 GI:7106156  
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Symplocarpus.

REFERENCE  
1 Ito, K.  
Isolation of two distinct cold-inducible cDNAs encoding plant  
uncoupling proteins from the spadix of skunk cabbage (Symplocarpus  
foetidus)  
Plant Sci. 149, 167-173 (1999)  
2 (bases 1 to 1525)  
Ito, K.  
Direct Submission  
Submitted (10-MAR-1999) Kikukatsu Ito, Cryobiosystem Research  
Center, Iwate Univ., Division of Biosystem and Bioresource  
Technology; 3-18-8, Ueda, Morioka 020-8550, Japan  
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Query Match	100.0%;	Score 1525;	DB 8;	Length 1525;		
Best Local Similarity	100.0%;	Fred. No. 0;				
Matches 1525;	Conservative	0;	Mismatches	0; Indels	0; Gaps	0;

  

QY	1	GAGGATTCGGAGAAGAGCCAGAACCGCATCTCTTCCGGCTCTCTCTCCTTCGCGCC	60
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QY	181	TCTTCTCTACATAAACCTCAACACCCCATCTCTCTCTCCGGCTTCGACACACCTGCAT	240
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QY	241	TCTACTGGAGGCCANTTGATCGAGGTTTTCCGGCGGAGATGGGGGATCACGGCCCGAG	300
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QY	301	ACCCAGATCTCGTTTTCGGCGGAGTTTCCGACGACGATTCGCGCGCTGTCTTCCGCGAGCT	360
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QY	361	TGCACGATTCGTTTGGACACTCTCTAAAGTTTAGGCTTCAACTCCAAAAGAACAGTAACA	420
Db	361	TGCACGATTCGTTTGGACACTCTCTAAAGTTTAGGCTTCAACTCCAAAAGAACAGTAACA	420
QY	421	GGTGATGTGGCGCTTTGCGGAATACAGGGGATGTGTGGGCACTGTGTGGCACTATTGGC	480
Db	421	GGTGATGTGGCGCTTTTGGCAAAATACAGGGGATGTGTGGGCACTGTGTGGCACTATTGGC	480
QY	481	ASGGAGGAGGTTTTCGCGACTCTGGAAGAGMATGTGACCGGTTTGCATCGTCGAATGC	540
Db	481	AGGAGGAGGTTTTCGCGACTCTGGAAGAGMATGTGACCGGTTTGCATCGTCGAATGC	540
QY	541	CTCTTTGGAGGCTACGAATTGGGTGTATGAACACAGTTAAGTCTCTTTATGTGTGGAGAT	600
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QY	601	AAC TTGTTGGAGATATTCCTTATCCAAGAAATACTTGCTGGGCTTACACAGGTGCA	660
Db	601	AAC TTGTTGGAGATATTCCTTATCCAAGAAATACTTGCTGGGCTTACACAGGTGCA	660
QY	661	TTAGCAATTATATAGTGGCAATCCCACTGACCTTGTAAAGTTCGACTTCAATCTGAAGGT	720
Db	661	TTAGCAATTATATAGTGGCAATCCCACTGACCTTGTAAAGTTCGACTTCAATCTGAAGGT	720
QY	721	AAACTCCCCCTCGGGGTACCGAGAGCTTATTACAGGGCGCTAAATGCTTATTCAAOCATA	780
Db	721	AAACTCCCCCTCGGGGTACCGAGAGCTTATTACAGGGCGCTAAATGCTTATTCAAOCATA	780

RESULT 4  
E50744  
LOCUS

LOCUS	2991 bp	DNA	linear	PAT 31-JAN-2002
E50744	E50744			



DEFINITION Plant exotherm-related gene and exotherm-related protein.  
 ACCESSION E50744  
 VERSION E50744.1 GI:18622140  
 KEYWORDS JP 200354489-A/2;  
 SOURCE Symplocarpus foetidus  
 ORGANISM Symplocarpus foetidus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Symplocarpus.  
 REFERENCE 1 (bases 1 to 2991)  
 AUTHORS Ito, K.  
 TITLE Plant exotherm-related gene and exotherm-related protein  
 JOURNAL SCIENCE & TECH AGENCY  
 COMMENT OS Symplocarpus foetidus  
 PN JP 200354489-A/2  
 PD 26-DEC-2000  
 PF 14-JUN-1999 JP 1999167439  
 PR  
 PI KIKUCHI ITO  
 PC C12N15/09, C07K14/415//A01H5/00, A61K31/00, A61K38/00,  
 C12P21/02,  
 PC C12N15/00, A61K37/02  
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 FT CDS (286)....(1089)  
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 Best Local Similarity 86.6%; Pred. No. 4.4e-263;  
 Matches 1357; Conservative 0; Mismatches 49; Indels 161; Gaps 9;  
 QY 1 GAGGATTCGAGAAAGGCCAGAACCGGATTCCTCCCGTCTCTCTCTCTCTCTCTCTCGCCC 60  
 DB 18 GAGGATTCGAGAAAGGCCAGAACCGGATTCCTCCCGTCTCTCTCTCTCTCTCTCTCGCCC 77  
 QY 61 AATTGCAGTTTTCGACGGGTCATCATCAGACCCCTCCGCTTTCCGGCCCAACGC 120  
 DB 78 AATTGCAGTTTTCGACGGG-GTCATCATCAGACCCCTCCGCTTTCCGGCCCAACGC 136  
 QY 121 CTTCCACCCCAACCAATCGCCCTCCGTTTCCGGAATATTCCTCTCTCTCTCTCTCTCTCT 180  
 DB 137 CTTCCACCC-----AATCCCTCCGTTTCCGGAATATTCGCTTC---CTCCCTTT 185  
 QY 181 TCTTCTCATATAACCTTAACA-CCCATCTCTCTCTCCGCTTTCCGACCAACCTGCA 239  
 DB 186 TCTTCTCATATAACCTTAACCAACCCCAATCTCTCTCTCCGCTTTCCGACCAACCTGCA 245  
 QY 240 TTCTACTGGAGCCCAATTGATCAGAGTTTCCCGGCGAGGATGGCGATCACGGCCCGAG 299  
 DB 246 TTCTACTGGAGTCCTTGTATCGAGCTTTCCCGGCGAGGATGGCGATCACGGCCCGAG 305

QY 300 GACCAGATCTCGTTTGGCGGAGTTCCGAGACAGCAITTCGCGCTTGTCTTCCCGAGCT 359  
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FH	Key	Location/Qualifiers
FT	CDS	(286)..(1089)
FT	polyA_site	(1171).
FT	polyA_site	(1176).
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<b>FEATURES</b>		
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<b>ORIGIN</b>		
Query Match      70.6%; Score 1076.6; DB 6; Length 2991;		
Best Local Similarity    86.6%; Pred. No. 4.4e-263;		
Matches 1357; Conservative    0; Mismatches 49; Indels 161; Gaps    9;		
QY	1	GAGGATTGCAGAGAAGGCCAGACCCGATTCCTTCCCGGTCTCTCTCCTTCCTTCCTTCGGCCC 60
DB	18	GAGGATTGCAGAGAAGGCCAGAACCCGATTCCTTCCCGGTCTCTCTCCTTCCTTCCTTCGGCCC 77
QY	61	AATTGCAGTTTTCGCAGCGCGGTCAATCAAGACCCTCGCGCTTTCGGCGCCMAAGCG 120
DB	78	AATTGCAGTTTTCGCAGCGG-GTCAATCATCAAGACCCTCGCGCTTTCGGCGCCMAAGCG 136
QY	121	CTTCCACCCCCACAATCGCCCTCGGTTTCCCGAATAATCTCTTCCTCTCTCCCTTT 180
DB	137	CTTCCACCC-----AATCCCTCGGTTTCCGAATAATTCCTCTTC--CTCCCTTT 185
QY	181	TCTTCTCTACATAAGCCGTACGA-CGCCATCTCTCTCCCGCTTCGACACCACTCGCA 239
DB	186	TCTTCTCTACATAAACTTAACACCCCACTCTCTCTCCCGCTTCGACACCACTCTGCA 245
QY	240	TTCTACTGGGAGCCCAATTGATCAGGTTTTCCCGCGAGGATGGCGGATCACGGCCCGAG 299
DB	246	TTCTACTGGGATCCCAATTGATCAGGTTTTCCCGCGAGGATGGCGGATCACGGCCCGAG 305
QY	300	GACCGAGATCTGTTTGCCGCGAGTTCGCGAGCAGCATTCGCCCGCTGCTTCGCGAGCT 359
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QY	360	TTGCAGCATTCGCTTGGAACCTGCTAAAGTTAGGCTTCAACTCCAAAAGAAAGACAGTAAC 419
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QY	420	AGGTGATGTGTGTGCTTGCCAAAATACAGGGGAATGTTGGGCACTGTTGCCACTATTGC 479
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240	TTCTACTGGAGACCATTGATCAGGTTTCCGCGAGAGATGGCGATCAGCGCCCGAG	299	TTCTACTGGAGATCCATTGATCGAGTTTCCGCGAGAGATGGCGATCAGCGCCCGAG
Qy		Db	
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Qy		Db	
360	TTGCAGATTCGCTTGACACTGCTAAAGTTAGGCTTCAACTCCAAAAGAAAGACAGTAAC	419	TTGCAGATTCGCTTGACACTGCTAAAGTTAGGCTTCAACTCCAAAAGAAAGACAGTAAC
Qy		Db	
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480	CAGCGGAGGAAGGTTTTCGGCACTCTGGAAGAGAAATGTATACCCGGTTTGCACTGCTAATG	539	CAGCGGAGGAAGGTTTTCGGCACTCTGGAAGAGAAATGTATACCCGGTTTGCACTGCTAATG
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486	CAGCGGAGGAAGGTTTTCGGCACTCTGGAAGAGAAATGTATACCCGGTTTGCACTGCTAATG	545	CAGCGGAGGAAGGTTTTCGGCACTCTGGAAGAGAAATGTATACCCGGTTTGCACTGCTAATG
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540	CCTCTTTGGAGGGCTAGCAATTCGGTTGTATGAACAGCTTAAGTCCTTTATTTGTGGAGA	599	CCTCTTTGGAGGGCTAGCAATTCGGTTGTATGAACAGCTTAAGTCCTTTATTTGTGGAGA
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546	CCTCTTTGGAGGGCTAGCAATTCGGTTGTATGAACAGCTTAAGTCCTTTATTTGTGGAGA	605	CCTCTTTGGAGGGCTAGCAATTCGGTTGTATGAACAGCTTAAGTCCTTTATTTGTGGAGA
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QY 600 TAACTTGTGGAGATATCTTTATCCAGAAATATCTTGGCTTACACAGGTGC 659  
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QY 1020 AGCTCAAAAGCACATTTGATTTGTTTCATCAAGACATTAATAATGATGGCTTCTTGC 1079  
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DEFINITION Symlocarpus foetidus mRNA for SFUCPb, complete cds.  
ACCESSION AB024734  
VERSION AB024734.1 GI:7106158  
KEYWORDS  
SOURCE  
ORGANISM  
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Symlocarpus foetidus  
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Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Symlocarpus.  
REFERENCE  
1  
Ito.K.  
TITLE Isolation of two distinct cold-inducible cDNAs encoding plant  
uncoupling proteins from the spadix of skunk cabbage (Symlocarpus  
foetidus)  
JOURNAL Plant Sci. 149, 167-173 (1999)  
REFERENCE 2 (bases 1 to 2991)  
AUTHORS Ito.K.  
TITLE Direct Submission  
JOURNAL Submitted (10-MAR-1999) Kikukatsu Ito, Cryobiosystem Research  
Center, Iwate Univ., Division of Biosystem and Bioresource  
Technology; 3-18-8, Ueda, Morioka 020-8550, Japan  
(E-mail:kikuito@iwate-u.ac.jp, Tel:81-19-621-6253)  
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Query Match 70.6%; Score 1076.6; DB 8; Length 2991;

	Best Local Similarity	86.6%;	Pred. No. 4.4e-263;	
	Matches 1357;	Conservative	0; Mismatches 49; Indels 161; Gaps	9;
Qy	1	GAGGATTCGCAAGAAAGCGACACCCGATTCCTTCCCGTCTCTCTCTCTCTCTCTCTCTCGGCC	60	
Db	18	GAGGATTCGCAAGAAAGCGACACCCGATTCCTTCCCGTCTCTCTCTCTCTCTCTCTCTCGGCC	77	
Qy	61	AAITGCAGTTTTTCGAGCGGCTCATATCAAGACCTTCGCTTTCGGCGCAACGC	120	
Db	78	AAITGCAGTTTTTCGAGCGG-GTCATCATCAAGACCTTCGCTTTCGGCGCAACGC	136	
Qy	121	CTTCCACCCCAACCAATCGCTCGTTTCCCGAAATATCTCTTCCTCTCTCTCTCTCTCTCT	180	
Db	137	CTTCCACCC-----AATCGCTCGTTCCCGAAATATCTCTCTCTCTCTCTCTCTCTCTCT	185	
Qy	181	TTCTCTCATATAAACCTTAACCA-CCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA	239	
Db	186	TTCTCTCTACATAAAACCTTAACCAACCCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA	245	
Qy	240	TTCTACTCGGAGCCCATTTGATTCAGGTTTCCGGGAGGATGGCGATCAGCGCCGAG	299	
Db	246	TTTACTTGGGATCCCATTTGATTCAGGTTTCCGGGAGGATGGCGATCAGCGCCGAG	305	
Qy	300	GACCGAGATCTCGTTTCCGCGAGTTTCGGGACGACATTCGCGCTTCTCTCTCTCTCTCTCTCTCTCT	359	
Db	306	GACCGAGATCTCGTTTCCGCGAGTTTCGGGACGACATTCGCGCTTCTCTCTCTCTCTCTCTCTCTCT	365	
Qy	360	TTGCACGATTCGTTTGGACACTGTTAAATTGCTTCAATCTCMAAAGAAAGAGTGATAC	419	
Db	366	CTGTACGATTCGTTTGGACACTGTTAAATTGCTTCAATCTCMAAAGAAAGAGTGATAC	425	
Qy	420	AGGTGATGTGGTGGCTTTCGMAAATACAGGGAATGTTGGGCACTGTTGCCACTATTGCT	479	
Db	426	AGGTGATGTGGTGGCTTTCGMAAATACAGGGAATGTTGGGCACTGTTGCCACTATTGCT	485	
Qy	480	CAGGAGGAAGGTTTTCGGCACTCTCGAAAGGAATGTATCCGGTTTCGATTCGTCATG	539	
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Qy	540	CCTCTTTGGAGGCTACGAATTTGGTTGTATGACACAGTTAAAGTCTTTTATGTTGACGA	599	
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Qy	660	ATTAGCAATATAGTGGCAATCCCACTGACTGTTTAAAGTTTCGACTTCAATCTGAAG	719	
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Db	846	TGCTATTATAAATCTGCTGAATTGGCCAGTTATGATCAAGTGAACA	893
Qy	900	ATTACACAGATCTCAGATAATATTTTACTCATATTTTAGCCGGTCTGGGGCAGGTT	959
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Db	981	TTTTTACAGGGGTTTATCCCAAACTTTGGTGGTGTAGATCGTGGGATGTGATCATGTT	1040
Qy	1140	TTTGACCTTTGAGACGAGTCACAAGATTTTTTCATCAAAGAGGTGCCAAATTAATACATGA	1199
Db	1041	TTTGACCTTTGAGACGAGTCACAAGATTTTTTCATCAAAGAGGTGCCAAATTAATACATGA	1100
Qy	1200	ACTCGGATAGGAGTAGAAGAAAGGGTTTTTGTGTGGAATTTCTCTACCGGTGTGATPCT	1259
Db	1101	AGTCGGATAGGAGTAGAAGAAAGGGTTTTTGTGTGGAATTTCTCTACCGGTGTGATPCT	1160
Qy	1260	GSCGAGAGACAAATAATCTCTCTGACTGCTCAGATG-TGTACCTTTTTTATGAATGGTT	1318
Db	1161	GSCGAGAGAGAAATAATCTCTCTGACTGCTCAGATGTTGTACCTTTTTATGAATGGTT	1219
Qy	1319	CTTTTCTTATAGGACAGAGAAAGAAA-AAAAAATCATTTGTCATTTACTCTTTTTCG	1377
Db	1220	CTTTTCTTATAGGACAGAGAGAAA-AAAAAGAAAATTCATTTGTCATCTCTTTTTCG	1279
Qy	1378	CCATTTCTGCTGCTATTC-----TT	1397
Db	1280	CCATTTCTGCTGAGTAGACGCTATACCAAGCAGACATTTTGTCTGGCTGCTGATATCT	1339
Qy	1398	GCTAGGAGAGAAAGTCTTACATTTGAGTGATACGTTGTCTCTGCATCCATATATTTT	1457
Db	1340	TGTAAGTGAAGAAAGTCTTACATTTGAGTGATACGTTGTCTCTGCATCCATATATTTT	1399
Qy	1458	CAGAGATCTATTTTGACATCAAGAAAGTAATGCATCAGGTTTTTTTTTAAAAA	1517
Db	1400	CAGAGTTACTATTTGACATCAAGAAAGTTTTTTTTTTTTTTTTTTTTTTTTAA	1459
Qy	1518	AAAAAA 1524	
Db	1460	AAATAGA 1466	

Search completed: June 5, 2004, 03:10:28  
Job time : 5865.22 secs

OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 16:54:52 ; Search time 571.031 Seconds  
(without alignments)  
11345.276 Million cell updates/sec

Title: US-10-671-628-1  
Perfect score: 1525  
Sequence: 1 gggattcgcagaagaagg.....taaaaaaaaaaaaaaaaa 1525

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04.\*  
1: Geneseqn1960s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002s.\*  
7: Geneseqn2003as.\*  
8: Geneseqn2003bs.\*  
9: Geneseqn2003cs.\*  
10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1525	100.0	1525	4 AAF77825	Aa77825 SfucPa de
2	1076.6	70.6	2991	4 AAF77826	Aa77826 SfucPa de
3	500.8	32.8	920	7 ADA68518	Ada68518 Arabidops
4	500.8	32.8	921	6 AB212956	Ab212956 Arabidops
5	500.8	32.8	1103	3 AAC46816	Aac46816 Arabidops
6	500.8	32.8	1225	5 AAS14822	Aa14822 Arabidops
7	473	31.0	1088	5 AAS14823	Aa14823 Arabidops

8	473	31.0	1224	3 AAC49402	Aac49402 Arabidops
9	471.4	30.9	1227	3 AAC33096	Aac33096 Arabidops
10	425.6	27.9	957	3 AAC49389	Aac49389 Arabidops
11	422.2	27.7	915	7 ADA70324	Ada70324 Rice Gene
12	415.4	27.2	974	5 AAS14825	Aa14825 Wheat cDN
13	321.8	21.1	825	7 ADA59501	Ada59501 Rice gene
14	167.4	11.0	471	3 AAC36817	Aac36817 Arabidops
15	163	10.7	1949	2 AAZ07061	Aaz07061 Mouse unc
16	163	10.7	1949	2 AAZ07061	Aaz07061 Mouse unc
17	163	10.7	1949	2 AAZ07061	Aaz07061 Mouse unc
18	163	10.7	1949	2 AAZ07061	Aaz07061 Mouse unc
19	160.6	10.5	1204	2 AAZ03119	Aaz03119 Mouse unc
20	160.6	10.5	1204	2 AAZ03119	Aaz03119 Mouse unc
21	159	10.4	1215	9 AAB52719	Aab52719 Primary r
22	159	10.4	1215	9 AAB52719	Aab52719 Primary r
23	159	10.4	1215	9 AAB52719	Aab52719 Primary r
24	159	10.4	1215	9 AAB52719	Aab52719 Primary r
25	159	10.4	1215	9 AAB52719	Aab52719 Primary r
26	156	10.2	930	2 AAZ9435	Aaz9435 UC22 Nucl
27	156	10.2	930	2 AAZ9435	Aaz9435 UC22 Nucl
28	156	10.2	1612	2 AAV44595	Aav44595 Human res
29	155.6	10.2	960	4 AAC83793	Aac83793 Hybrid hU
30	154.4	10.1	930	2 AAZ19968	Aaz19968 Human unc
31	154.4	10.1	930	2 AAZ19968	Aaz19968 Human unc
32	154.4	10.1	1024	7 ABZ83760	Abz83760 Toxiciolog
33	154.4	10.1	1105	2 AAZ9434	Aaz9434 UC22 Nucl
34	154.4	10.1	1105	2 AAZ9434	Aaz9434 UC22 Nucl
35	154.4	10.1	1105	2 AAZ9434	Aaz9434 UC22 Nucl
36	154.4	10.1	1105	2 AAZ9434	Aaz9434 UC22 Nucl
37	154.4	10.1	1643	6 AAS94928	Aas94928 Human DNA
38	152.8	10.0	1255	2 AAZ09078	Aaz09078 Human DNA
39	152.8	10.0	1596	2 AAZ82381	Aaz82381 Full leng
40	152.8	10.0	1596	2 AAZ82381	Aaz82381 Full leng
41	152.8	10.0	1596	2 AAZ82381	Aaz82381 Full leng
42	152.8	10.0	1596	2 AAZ82381	Aaz82381 Full leng
43	152.8	10.0	1882	3 AAZ29244	Aaz29244 Human mit
44	152.8	10.0	1888	2 AAZ9436	Aaz9436 UC22 Nucl
45	152.8	10.0	1888	6 AEX84483	Abk84483 Human cDN

ALIGNMENTS

RESULT 1

AAAF77825

ID AAF77825 standard; cDNA; 1525 BP.

XX

AC AAF77825;

XX

DT 29-MAY-2001 (first entry)

XX

DE SfucPa derived exothermicity relating gene coding sequence #1.

XX

XW SfucPa derived exothermicity relating gene; diabetes; obesity;

XX exothermic material; low temperature resistant plant; ss.

OS Symplocarpus foetidus.

XX

PN JP2000354489-A.

XX

PD	26-DEC-2000.
XX	
FF	14-JUN-1999; 99JP-00167439.
XX	
PR	14-JUN-1999; 99JP-00167439.
XX	
PA	(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX	
DR	WPI: 2001-260368/27.
XX	P-PSDB; AAB73297.
XX	
XX	Exothermicity relating genes and proteins, useful in the treatment of diabetes and obesity.
PT	
XX	Claim 1; Page 6-7; 15pp; Japanese.
PS	
CC	The present sequence is the coding sequence for a Symptlocarpus foetidus (SFUCA) derived exothermicity relating gene. The gene is useful for preparation of low temperature resistant plants, and in the treatment of diabetes and obesity. The encoded protein is useful as exothermic materials for industrial use
CC	
XX	Sequence 1525 BP; 398 A; 341 C; 334 G; 452 T; 0 U; 0 Other;
SX	
Qy	Query Match 100.0%; Score 1525; DB 4; Length 1525; Best Local Similarity 100.0%; Pred. No. 0; Matches 1525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 GAGGATTGGCGAAGAAAGGCAGACCGCATTCCTTCCCGTCTCTCTCCTTCGCCCC 60 
Db	1 GAGGATTGGCGAAGAAAGGCAGAACCGATTCCTTCCCGTCTCTCTCCTTCGCCCC 60 
Qy	61 AAATTGACAGTTTTTCGACGCGCGGTCAATCAAGACCCTTCGCGCTTTCCGGGCCAAAGC 120 
Db	61 AAATTGCAGTTTTTCGACGCGCGGTCAATCAAGACCCTTCGCGCTTTCCGGGCCAAAGC 120 
Qy	121 CTTCACCCCCACCCAATCGCTCGCTTGCGGAATAATGCTCTTCCTTCCTTCCTTT 180 
Db	121 CTTCACCCCCACCCAATCGCTCGCTTGCGGAATAATGCTCTTCCTTCCTTCCTTT 180 
Qy	181 TCTTCTCTACATAAACCCCTTAACAACCCCATCTCTCTCCCGCTTCGACACACCTGCAT 240 
Db	181 TCTTCTCTACATAAACCCCTTAACAACCCCATCTCTCTCCCGCTTCGACACACCTGCAT 240 
Qy	241 TCTACTGGAGSCCAHTTGATCGAGGTTTCCGGCGAGATGGGCGATCAOGGCCGAGS 300 
Db	241 TCTACTGGAGSCCAHTTGATCGAGGTTTCCGGCGAGATGGGCGATCAOGGCCGAGS 300 
Qy	301 ACCGAGATCTGGTTTTCGGCGAGTTTCGCGAGCAGCATTCGCGGCTTGCTTGGCGGAGCTT 360 
Db	301 ACCGAGATCTGGTTTTCGGCGAGTTTCGCGAGCAGCATTCGCGGCTTGCTTGGCGGAGCTT 360 
Qy	361 TGACAGATTCCGTTTGACACTCTTAAGTAGGCTTCACTTCGAAAAGAACGAGTAACA 420 
Db	361 TGACAGATTCCGTTTGACACTCTTAAGTAGGCTTCACTTCGAAAAGAACGAGTAACA 420 
Qy	421 GGTCATGTCGGTGGCTTGGCAAAATACAGGGGAATGTGGGCACTGTGCCACTATTGCC 480 

[illegible]

Db 1261 GCGAGACAAATAATCTCTGCTGCTCAGATGTGTACCTTTTATGATGTTCT 1320  
QY 1321 TTCTTATAGACGACAGAGAAAGAAAAAATCATGTGCACTTTTCTTTTCCCA 1380  
Db 1321 TTCTTATAGACGACAGAGAAAGAAAAAATCATGTGCACTTTTCTTTTCCCA 1380  
QY 1381 TTCTGCTGCTAATCTTGGTAGAGAGAAAGCTTTACATTGAGTGATACGTTGTTCT 1440  
Db 1381 TTCTGCTGCTAATCTTGGTAGAGAGAAAGCTTTACATTGAGTGATACGTTGTTCT 1440  
QY 1441 CTGCATCCATTATTTTCAGAGATACTATTTGACACATGAAAAAGTAATGCACATCAGGTT 1500  
Db 1441 CTGCATCCATTATTTTCAGAGATACTATTTGACACATGAAAAAGTAATGCACATCAGGTT 1500  
QY 1501 TTTTAAAAAAGAAAAAAGAAAAA 1525  
Db 1501 TTTTAAAAAAGAAAAAAGAAAAA 1525

Search completed: June 4, 2004, 22:21:07  
Job time : 576.031 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 21:05:07 ; Search time 3860.45 Seconds  
(without alignments)  
11796.502 Million cell updates/sec

Title: US-10-671-628-1  
Perfect score: 1525  
Sequence: 1 gaggattcgcagagaag9.....taaaaaaaaaaaaaaaaaa 1525

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_nam:\*  
23: em\_gss\_nus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*

28: gb\_gss1:\*  
29: gb\_gss2:\*

Search completed: June 5, 2004, 06:21:11  
Job time : 3866.45 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			Description
		Match	Length	ID	
1	540.4	35.4	1241	14	CB330501
2	516.2	33.8	871	14	CB290646
3	446.6	29.3	1447	13	BUI03700
4	443	29.0	797	13	BQ743348
5	437.2	28.7	1422	11	AY105357
6	429.2	28.1	779	14	CF448435
7	425.8	27.9	746	14	CF089986
8	425	27.9	660	12	BI096046
9	423.2	27.8	878	14	CD433462
10	404.2	26.5	712	14	CF452690
11	403.6	26.5	719	14	CF445646
12	397	26.0	894	14	CB290645
13	396.4	26.0	1085	14	CK207934
14	394	25.8	762	14	CF213174
15	391.4	25.7	746	14	CD921168
16	390.8	25.6	832	10	B5642116
17	390.6	25.6	742	14	CB648044
18	388	25.4	670	9	AJ432883
19	386.2	25.3	733	13	BQ972958
20	376.8	24.7	670	14	CF810597
21	373	24.5	695	14	CB648002
22	367.2	24.1	756	13	CA086808
23	367	24.1	682	14	CF436214
24	361.6	23.7	649	14	CF442797
25	360.8	23.7	768	12	B6321351
26	357	23.4	610	13	BQ967986
27	355.8	23.3	872	12	BG446588
28	353.6	23.2	766	13	B0483475
29	352	23.1	1153	14	CK209055
30	341.6	22.4	994	12	BG416382
31	337.2	22.1	747	14	CD841700
32	337	22.1	817	14	CD447945
33	333	21.8	821	10	B6641808
34	332	21.8	679	12	BG450507
35	331.4	21.7	598	13	B0916601
36	329.8	21.6	769	14	CD829664
37	329	21.6	714	12	BJ283810
38	326.2	21.4	603	10	BF727999
39	325.2	21.3	692	13	BQ969842
40	324.6	21.3	628	10	AW330667
41	324.6	21.3	643	14	CA271689
42	323.8	21.2	506	13	B0106121
43	322	21.1	678	13	BQ909270
44	322	21.1	709	13	BQ842169
45	319.4	20.9	798	14	CD433355



OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 16:59:57 ; Search time 11489.8 Seconds

Title: US-10-671-628-3

Perfect score: 2991

Sequence: 1 tgggtgacagtgacgag.....ccagccagtaaaaaaaaaa 2991

(without alignments)

11282.980 Million cell updates/sec

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

15: em.ba.\*

16: em.fun.\*

17: em.hum.\*

18: em.in.\*

19: em.mu.\*

20: em.om.\*

21: em.ox.\*

22: em.ov.\*

23: em.pat.\*

24: em.ph.\*

25: em.pl.\*

26: em.ro.\*

27: em.sts.\*

28: em.un.\*

29: em.vi.\*

30: em.htg\_hum.\*  
31: em.htg\_inv.\*  
32: em.htg\_other.\*  
33: em.htg\_mus.\*  
34: em.htg\_pin.\*  
35: em.htg\_rdi.\*  
36: em.htg\_mam.\*  
37: em.htg\_vrt.\*  
38: em.sy.\*  
39: em.htgo\_hum.\*  
40: em.htgo\_mus.\*  
41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB ID	Description
		Match	Length	%		
1	2991	100.0	2991	6	ES0744	ES0744 Plant exoth
2	2991	100.0	2991	6	BD011856	BD011856 Thermogen
3	2991	100.0	2991	8	AB024734	AB024734 Symplocar
4	1076.6	36.0	1525	6	ES0743	ES0743 Plant exoth
5	1076.6	36.0	1525	6	BD011855	BD011855 Thermogen
6	1076.6	36.0	1525	8	AB024733	AB024733 Symplocar
7	456.8	15.3	1209	8	AB088762	AB088762 Hellicodic
8	374.6	12.5	1429	8	AF472619	AF472619 Lycopersi
9	368.2	12.3	1434	8	STUCPMRNA	Y11220 Solanum tub
10	347.4	11.6	920	6	AX651736	AX651736 Sequence
11	347.4	11.6	921	6	AX506066	AX506066 Sequence
12	347.4	11.6	921	8	AF146226	AF146226 Arabidops
13	347.4	11.6	952	8	AY091185	AY091185 Arabidops
14	347.4	11.6	1274	8	AY056272	AY056272 Arabidops
15	339.4	11.3	1240	8	ATMTUNCOU	AJ001264 Arabidops
16	337.8	11.3	1225	6	AX269361	AX269361 Sequence
17	337.8	11.3	1225	8	ATFUMP	AJ223983 Arabidops
18	320.4	10.7	1088	6	AX269362	AX269362 Sequence
19	320.4	10.7	1088	8	AB021706	AB021706 Arabidops
20	318.8	10.7	1227	8	AY088200	AY088200 Arabidops
21	310	10.4	1376	8	BT009306	BT009306 Triticum
22	273.2	9.1	1243	8	AF461732	AF461732 Zea mays
23	272.8	9.1	1263	8	AK061318	AK061318 Oryza sat
24	271.2	9.1	1179	8	AK104090	AK104090 Oryza sat
25	251.8	8.4	915	6	AX653777	AX653777 Sequence
26	241.8	8.1	974	6	AX269364	AX269364 Sequence
27	241.8	8.1	974	8	AB042428	AB042428 Triticum
28	238.6	8.0	971	8	AB042429	AB042429 Triticum
29	178.4	6.0	1405	8	AK102326	AK102326 Oryza sat
30	178.4	6.0	1451	8	AK103874	AK103874 Oryza sat
31	156.8	5.2	825	6	AX652954	AX652954 Sequence
32	156.2	5.2	1703	8	AY251055	AY251055 Anthurium
33	153.2	5.1	1157	8	AF343446	AF343446 Actinidia
34	150	5.0	777	8	ACTACTB	M21336 Actinidia d

C 35	150	5.0	809	8	ACACT7	X12139 Actindia c
C 36	150	5.0	1370	8	ACIND	X1466 Actindia d
C 37	149.6	5.0	1361	8	VCISPERO	X75749 V.sativa b.
C 38	145.8	4.9	1337	8	ACTACTA	M21335 Actindia d
C 39	145.8	4.9	1338	8	ACTACTA	X13013 Actindia c
C 40	143.4	4.8	1830	8	AF019147	AF019147 4a mayas
C 41	142	4.7	1751	8	AF259983	AF259983 Ipomoea b
C 42	141.6	4.7	1659	8	AF454957	AF454957 Brassica
C 43	140.6	4.7	6428	8	AC269360	AC269360 Sequence
C 44	140.6	4.7	6428	8	STA22586	AF002586 Solarium t
C 45	138.6	4.6	1828	8	AB020961	AB020961 4a mayas

## ALIGNMENTS

RESULT 1	
ES0744	LOCUS
ES0744	2991 bp DNA linear PAT 31-JAN-2002
DEFINITION	Plant exotherm-related gene and exotherm-related protein.
ACCESSION	ES0744
VERSION	ES0744.1 GI:18622140
KEYWORDS	JP 2000354489-A/2.
SOURCE	Symplocarpus foetidus
ORGANISM	Symplocarpus foetidus
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Symplocarpus.
REFERENCE	1 (bases 1 to 2991)

INVENTOR	ITO, K.
ATTORNEY	Plant exotherm-related gene and exotherm-related protein
TITLE	Patent: JP 2000354489-A 2 26-DEC-2000;
JOURNAL	SCIENCE & TECH AGENCY
	COMMENT
	OS Symlocarpus foetidus
	PN JP 2000354489-A/2
	PD 26-DEC-2000
	PF 14-JUN-1999 JP 1999167439
	PR
	PI KIKUCHI ITO
	PC C12N5/09, C07K14/415//A01H5/00,A61K31/00,A61K38/00,

FEATURE	source
PH	Key
FT	CDS
FT	polyA_site
FT	polyA_site
	Location/Qualifiers
	1..2891
	/organism="Symplectcarpus foetidus"
	/mol_type="genomic DNA"
	/db_xref="taxon:28477"
	Location/Qualifiers
	(286)..(1089)
	(1171)..(1176)
	(1243)..(1248)

```

ORIGIN
      100.00; Score 3991; DB 6; Length 2991;
      Best Local Similarity 100.00; Pred. No. 0;
      Matches 2991: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 TGGTGGTGACGAGTGCAGGAGTTCCGAGAAGAAAGGCCAGAACCCGATTCTTCCCGTC 60  
|||||

Db 1 TGGTGGTGACGAGTGCAGGAGTTCCGAGAAGAAAGGCCAGAACCCGATTCTTCCCGTC 60  
|||||

QY 901 TCTAGATGATGGGAGTTTACGCTACAAAAGCACAATTTGATTTTTCATCAAGAGTTTG 960  
DB 901 TCTAGAAATGATGGGAGATTCAGCTTACAAAAGCACAATTTGATTTTTCATCAAGAGTTTG 960  
QY 961 AAAAATCATGGGCTCTTGCTTTTACAGGGTTTATCCCAAACTTTTGGTCGGTTAGCA 1020  
DB 961 AAAAATGATGGGCTCTTGCTTTTACAGGGTTTATCCCAAACTTTTGGTCGGTTAGCA 1020  
QY 1021 TCGTGGAAATGATCATGTTTGTGACCTTGGAGCAGGTCAAGAAATTTCTTCAACAAAG 1080  
DB 1021 TCGTGGAAATGATCATGTTTGTGACCTTGGAGCAGGTCAAGAAATTTCTTCAACAAAG 1080  
QY 1081 GTGCGAAAATTAATCATTTGAAGTCGGATAGGATAGAAAAGGGTTTGTGGAAATT 1140  
DB 1081 GTGCGAAAATTAATCATTTGAAGTCGGATAGGATAGAAAAGGGTTTGTGGAAATT 1140  
QY 1141 TCTCTACCGGTGTCGATTCCTGGCAGAGATAAATCTTCTGACTGCTCAGATGTTG 1200  
DB 1141 TCTCTACCGGTGTCGATTCCTGGCAGAGATAAATCTTCTGACTGCTCAGATGTTG 1200  
QY 1201 ACCTTTTATGATGCTTTCTTTCTATAGAGCAGAGAAATTAAGAAAATTCAT 1260  
DB 1201 ACCTTTTATGATGCTTTCTTTCTATAGAGCAGAGAAATTAAGAAAATTCAT 1260  
QY 1261 TGTCTGTACTCTTTTCCCAATTTCTGCTGAGTAGCAGCTATACCAAGCAGACTTTGTT 1320  
DB 1261 TGTCTGTACTCTTTTCCCAATTTCTGCTGAGTAGCAGCTATACCAAGCAGACTTTGTT 1320  
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DB 1321 GCTTGGCTGCTGCTAATCTTGTAGCTGAAGAAATCTTACATGAGTGAATAGCTTTGTT 1380  
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QY	61 TTCTCTCTCTCCGCCCAATTGCAGTTTTCGAGCGGTCATCATCAGACCCCTCGCC 120
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QY	121 TTTCGCGCCAAAGCGCTTCACCCCAATCCCTCGGTTTCCGAAATATTCGCCCTTCCTC 180
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QY	541 CAATGCGCTCTTGGAGGCGTACGAATTTGGGTTGTATGACACGATTAAAGTCCTTTATGTT 600
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BD011856			
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JOURNAL REFERENCE	Plant Sci. 149, 167-173 (1999)
AUTHORS	Ito, K.
TITLE	Direct Submission
JOURNAL	Submitted (10-MAR-1999) Kikukatsu Ito, Cryobiosystem Research Center, Iwate Univ., Division of Biosystem and Bioresource Technology; 3-18-8, Ueda, Morioka 020-8550, Japan (E-mail:kikuito@wate-u.ac.jp, Tel:81-19-621-6253)
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Db 2821 TGGACAGATCTCGAGGTGAAGAGGTTCCGGCGGCGGTGCTCGGTGCGGATGTCAGC 2880  
Qy 2881 ATGATGTAATTTCCAGTTGTTAGTGAATAACCATGTCATTCGTGTAAGTCTTTTCG 2940  
Db 2881 ATGATGTAATTTCCAGTTGTTAGTGAATAACCATGTCATTCGTGTAAGTCTTTTCG 2940



OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 16:54:52 ; Search time 1119.97 Seconds  
(without alignments)

11345.276 Million cell updates/sec

Title: US-10-671-628-3

Perfect score: 2991

Sequence: 1 tggctggagcgtgacag.....ccggccagtaaaaaaaaaa 2991

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001as:\*

5: Geneseq2001bs:\*

6: Geneseq2002as:\*

7: Geneseq2003as:\*

8: Geneseq2003bs:\*

9: Geneseq2003cs:\*

10: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2991	100.0	2991	4 AAF77826	Aaf77826 SfUCPa de
2	1076.6	36.0	1525	4 AAF77825	Aaf77825 SfUCPa de
3	347.4	11.6	920	7 ADA68518	Ada68518 Arabidops
4	347.4	11.6	921	6 AB212956	Ab212956 Arabidops
5	347.4	11.6	1103	3 AAC46816	Aac46816 Arabidops
6	337.8	11.3	1225	5 AAS14822	Aas14822 Arabidops
7	320.4	10.7	957	3 AAC49389	Aac49389 Arabidops
8	320.4	10.7	1088	5 AAS14823	Aas14823 Arabidops

9	320.4	10.7	1224	3 AAC49402	Aac49402 Arabidops
10	318.8	10.7	1227	3 AAC33096	Aac33096 Arabidops
11	251.8	8.4	915	7 ADA70324	Ada70324 Rice gene
12	241.8	8.1	974	5 AAS14825	Aas14825 Wheat CDN
13	167.4	5.6	471	3 AAC36817	Aac36817 Arabidops
14	166.8	5.2	825	7 ADA9501	Ada9501 Rice gene
c 15	141.8	4.7	1879	3 AAC44552	Aac44552 Zea mays
c 16	140.6	4.6	282	6 ABL76423	Ab176423 S. tubero
c 17	138.2	4.6	6428	5 AAS14821	Aas14821 S. tubero
c 18	137.8	4.6	1645	2 AAV82458	Av82458 Triticum
c 19	136.2	4.6	1202	8 ADA48993	Ada48993 Wheat Gen
c 20	136.2	4.6	1392	6 AB213567	Ab213567 Arabidops
c 21	134.8	4.5	1407	8 ADA49223	Ada49223 Maize Gen
c 22	133.2	4.5	1056	2 AAT79545	Aat79546 Glycine m
c 23	131.6	4.4	1056	2 AAT74043	Aat74043 Soybean t
c 24	131.6	4.4	1392	6 ABN83213	Abn83213 Soybean D
c 25	131.6	4.4	1392	7 AAL50308	Aal50308 Soybean t
c 26	131.6	4.4	1849	2 AAT74042	Aat74042 Soybean t
c 27	130	4.3	1807	2 AAT74041	Aat74041 Soybean t
c 28	129.8	4.3	816	6 ABQ3882	Abq3882 Human unc
c 29	129	4.3	1463	4 AAF44787	Aaf44787 Cysteine
c 30	129	4.3	1463	9 ADB94728	Adb94728 Programme
c 31	128.6	4.3	1017	2 AAT68956	Aat68956 Blackcurr
c 32	127.4	4.3	1600	4 AAF44793	Aaf44793 Cysteine
c 33	127.4	4.3	1600	9 ADB94734	Adb94734 Programme
c 34	126.4	4.2	1474	2 AAT90174	Aat90174 Oil seed
c 35	126.2	4.2	557	4 AAF44798	Aaf44798 Cysteine
c 36	126.2	4.2	557	9 ADB94739	Adb94739 Programme
c 37	126.2	4.2	1390	2 AAT90171	Aat90171 Oil seed
c 38	126.2	4.2	1434	2 AAT90172	Aat90172 Oil seed
c 39	126.2	4.2	1441	2 AAT90173	Aat90173 Oil seed
c 40	126.2	4.2	1776	9 ADB94872	Adb94872 Programme
c 41	125.8	4.2	886	4 AAF44789	Aaf44789 Cysteine
c 42	125.8	4.2	886	9 ADB94730	Adb94730 Programme
c 43	124	4.1	1317	7 ADA70847	Ada70847 Rice gene
c 44	124	4.1	1317	8 ADA48729	Ada48729 Rice gene
c 45	123.6	4.1	910	2 AAV66759	Aav66759 Pathogen

ALIGNMENTS

RESULT 1

AAf77826

ID AAF77826 standard; cDNA; 2991 BP.

XX

AC AAF77826;

XX

DT 29-MAY-2001 (first entry)

XX

DE SfUCPa derived exothermicity relating gene coding sequence #2.

XX

KW SfUCPa derived exothermicity relating gene; diabetes; obesity;

XX exothermic material; low temperature resistant plant; ss.

OS Symlocarpus foetidus.

XX

FN JP2000354489-A.

XX

PD 26-DEC-2000.

XX PF 14-JUN-1999; 99JP-00167439.  
XX PR 14-JUN-1999; 99JP-00167439.  
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX DR WPI; 2001-260368/27.  
XX DR P-PSDB; AAB73298.  
XX PT Exothermicity relating genes and proteins, useful in the treatment of  
XX PT diabetes and obesity.  
XX PS Claim 2; Page 8-10; 15pp; Japanese.  
XX CC The present sequence is the coding sequence for a Symlocarpus foetidus  
XX CC (SfUCPa) derived exothermicity relating gene. The gene is useful for  
XX CC preparation of low temperature resistant plants, and in the treatment of  
XX CC diabetes and obesity. The encoded protein is useful as exothermic  
XX CC materials for industrial use  
XX SQ Sequence 2991 BP; 739 A; 716 C; 695 G; 841 T; 0 U; 0 Other;  
Query Match 100.0%; Score 2991; DB 4; Length 2991;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2991; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TGGTGGTACGAGTACGAGGATTGCGAAGAAAGGCCAGAACCCGATTCTTCCCGTC 60  
DB 1 TGGTGGTACGAGTACGAGGATTGCGAAGAAAGGCCAGAACCCGATTCTTCCCGTC 60  
QY 61 TTCTTCTCCTTCGCGCAATTCGAGTTTTCGAGCGGGTTCATCAAGACCTCCGCC 120  
DB 61 TTCTTCTCCTTCGCGCAATTCGAGTTTTCGAGCGGGTTCATCAAGACCTCCGCC 120  
QY 121 TTTCGCGCAAGCCCTTCCACCAATCCCTCCGTTTCCCGAAATATTCGCCCTTCCCTC 180  
DB 121 TTTCGCGCAAGCCCTTCCACCAATCCCTCCGTTTCCCGAAATATTCGCCCTTCCCTC 180  
QY 181 CTTTTCCTCTACATAAACCTTAACACCCGATCTCTCTCCGCTTCGACAC 240  
DB 181 CTTTTCCTCTACATAAACCTTAACACCCGATCTCTCTCCGCTTCGACAC 240  
QY 241 CTGCATCTACTGGGATCCCATTTGATCGACGTTTCCCGGAGGATGGCGATCAAGC 300  
DB 241 CTGCATCTACTGGGATCCCATTTGATCGACGTTTCCCGGAGGATGGCGATCAAGC 300  
QY 301 CCGAGGACCGAGATCTCGTTTCGCGGAGTTTCGCGAGCAGCATTCGCCCTTCGTC 360  
DB 301 CCGAGGACCGAGATCTCGTTTCGCGGAGTTTCGCGAGCAGCATTCGCCCTTCGTC 360  
QY 361 GAGCTCTGTACGATTCGGTTCGACACTGCTTAAGTTAGGCTTCAGTCCAAAGAAAGCA 420  
DB 361 GAGCTCTGTACGATTCGGTTCGACACTGCTTAAGTTAGGCTTCAGTCCAAAGAAAGCA 420  
QY 421 GTAAAGGTGATGTGGTGGCTTTCGCAAAATACAGGGCAATGTGGGCACTGTGGCACT 480  
DB 421 GTAAAGGTGATGTGGTGGCTTTCGCAAAATACAGGGCAATGTGGGCACTGTGGCACT 480

DB 421 GTAAAGGTGATGTGGTGGCTTTCGCAAAATACAGGGCAATGTGGGCACTGTGGCACT 480  
QY 481 ATTTGCCAGGAGGAAGGTTTGTGGCACTCTCGAAAGGAATTTGTACCGGTTTGCATCGT 540  
DB 481 ATTTGCCAGGAGGAAGGTTTGTGGCACTCTCGAAAGGAATTTGTACCGGTTTGCATCGT 540  
QY 541 CAATGCCCTCTTTGGAGGCTACGAAATGGGTTGTATGAACAGTTTAAGTCTTTTATGTT 600  
DB 541 CAATGCCCTCTTTGGAGGCTACGAAATGGGTTGTATGAACAGTTTAAGTCTTTTATGTT 600  
QY 601 GGAGTAACTTTGTTGGAGATATTCCTTTATCCAGAAATATCTTGTGGGCTTACACA 660  
DB 601 GGAGTAACTTTGTTGGAGATATTCCTTTATCCAGAAATATCTTGTGGGCTTACACA 660  
QY 661 GGTGCATTAGCAATTATAGTGGCAATCCGACTGACCTTGTAAAGTTTCGACTTCAATCT 720  
DB 661 GGTGCATTAGCAATTATAGTGGCAATCCGACTGACCTTGTAAAGTTTCGACTTCAATCT 720  
QY 721 GAAGTAACTCCCCCTGGGTTACCAAGAGATTATTCAGGGGCGCTAAATGCTTATTC 780  
DB 721 GAAGTAACTCCCCCTGGGTTACCAAGAGATTATTCAGGGGCGCTAAATGCTTATTC 780  
QY 781 ACCATAGTCAAAAGGAAGGACTTGGTCTCTGTGACTGGGCTTGTCTCTAATATTCGC 840  
DB 781 ACCATAGTCAAAAGGAAGGACTTGGTCTCTGTGACTGGGCTTGTCTCTAATATTCGC 840  
QY 841 CGAATGCTATTATAAATGCTGCTGAATTTGGCCAGTTATGATCAAGTGAACAGATGAAG 900  
DB 841 CGAATGCTATTATAAATGCTGCTGAATTTGGCCAGTTATGATCAAGTGAACAGATGAAG 900  
QY 901 TCTAGAAATGATGGAGATTTCAGCTACAAAGCCACATTTGATTGTTTTCATCAGACGTTG 960  
DB 901 TCTAGAAATGATGGAGATTTCAGCTACAAAGCCACATTTGATTGTTTTCATCAGACGTTG 960  
QY 961 AAAAAATGATGGGCTCTTGTCTTTTACAAGGGGTTTATCCCAAACTTTGGTCGTTAGGA 1020  
DB 961 AAAAAATGATGGGCTCTTGTCTTTTACAAGGGGTTTATCCCAAACTTTGGTCGTTAGGA 1020  
QY 1021 TGGTGAATGATCATGATTTTGAACCTTGGAGCAGGTCAAGAGTTCTTCATCAAGAG 1080  
DB 1021 TGGTGAATGATCATGATTTTGAACCTTGGAGCAGGTCAAGAGTTCTTCATCAAGAG 1080  
QY 1081 GTGCCAAATTAATACATTTGAATCGGATAGGATAGAAAAAAGGGTTTTTGTGAAATTT 1140  
DB 1081 GTGCCAAATTAATACATTTGAATCGGATAGGATAGAAAAAAGGGTTTTTGTGAAATTT 1140  
QY 1141 TCTCTACCGGTGTGATCTTGGCGAGAGAAATTAATCTTCTGACTGCTCAGATGTTGT 1200  
DB 1141 TCTCTACCGGTGTGATCTTGGCGAGAGAAATTAATCTTCTGACTGCTCAGATGTTGT 1200  
QY 1201 ACCTTTTATGAATGTTCTTTTCTTATAGAGCAGAGAAATTAAGAAAAATTCAT 1260  
DB 1201 ACCTTTTATGAATGTTCTTTTCTTATAGAGCAGAGAAATTAAGAAAAATTCAT 1260  
QY 1261 TGTCTATGTTACTCTTTTTCGCCATTTCTGCTGAGTAGCAGCTATACCAAGCAGACTTTGTT 1320  
DB 1261 TGTCTATGTTACTCTTTTTCGCCATTTCTGCTGAGTAGCAGCTATACCAAGCAGACTTTGTT 1320

Qy	2161	ACATTTTCATACGATCAATCGAGGTGACCTTAAATAGANNITGCTTCGCAAGTTCCTCGA	2220
Db	2161	ACATTTTCATACGATCAATCGAGGTGACCTTAAATAGANNITGCTTCGCAAGTTCCTCGA	2220
Qy	2221	CGTCCCTGTGTACGGGTAAATTTTTGAAAAAGAGAGAGCGCGGAAGAAAGCCGCGTCTCT	2280
Db	2221	CGTCCCTGTGTACGGGTAAATTTTTGAAAAAGAGAGAGCGCGGGAAGAGCCGCGTCTCT	2280
Qy	2281	GCTCGGACGCGGTTAAATTCCTCATATGCGCACTTCCA	2340
Db	2281	GCTCGGACGCGGTTAAATTCCTCATATGCGCACTTTCGATGAGCTTTCGCGAGCCTCCAGC	2340
Qy	2341	TTGGTTCTCACTCGCGCTCCCTCCACACACAGCCGCTTCCCGCTCGCGCTCTCTTCTTC	2400
Db	2341	TTGGTTCTCACTCGCGCTCCCTCCACACAGCGGTTTCCCGCTTCGCGCTCTCTTCTTC	2400
Qy	2401	CCAGGGTCGCAAGAGGCTCGTGTGTTGCGGGCGGAGAACCCGCGAGCAACCCCGCCGCC	2460
Db	2401	CCAGGGTCGCAAGAGGCTCGTGTGTTGCGGGCGGAGGAAGCGCGAGCAACCCCGCCGCC	2460
Qy	2461	CGGCGCGCGGAGGGAGCGCGCGCGCGCCGCCAAGCGCGACCCGATCGGGGCCAAGAG	2520
Db	2461	CGGCGCGCGGAGGGAGCGCGCGCGCGCCGCCAAGCGCGCAACCGATCGGGGCCAAGAG	2520
Qy	2521	GGGCTCAAGAGTTCATATAGTCTTAATTTCTTTCCGCTGTGGTCTCTCGAGTTAGAT	2580
Db	2521	GGGCTCAAGAGTTCATATAGTCTTAATTTCTTTCCGCTGTGGCTCTCTCGAGTTAGAT	2580
Qy	2581	TTGTTTCCCTCTCTCTTTTGTGTGTTTTCAAATTTAAATTTATCTCATCTGTG	2640
Db	2581	TTGTTTCCCTCTCTCTTTTGTGTGTTTTCAAATTTAAATTTATCTCATCTGTG	2640
Qy	2641	GACGACCTTCATCGGGTTTTGTCCTCTTCGAGGTGAGATCTTCGGAGGAAATCTCT	2700
Db	2641	GACGACCTTCATCGGGTTTTGTCCTCTTCGAGGTGAGATCTTCGGAGGAAATCTCT	2700
Qy	2701	ACTGGTTCAAACGGTGTGCGATCGGTGGTGTTCACAGGATCCGCGCACTCGATACC	2760
Db	2701	ACTGGTTCAAACGGTGTGCGATCGGTGGTGTGTGATCAGGATCCGCGCACTCGATACC	2760
Qy	2761	CGGTCGTGGTTTCCAAAGGTCAACTATGCGAAAGCTCTCGACAAACAACTACGCAAC	2820
Db	2761	CGGTCGTGGTTTCCAAAGGTCAACTATGCGAAAGCTCTCGACAAACAACTACGCAAC	2820
Qy	2821	TGACACAGATCCTCGAGGTGAATGAGGTCGCGGGCGCTGGTTCGGGCACTGTCAGC	2880
Db	2821	TGACACAGATCCTCGAGGTGAATGAGGTCGCGGGCGCTGGTTCGGGCACTGTCAGC	2880
Qy	2881	ATGATGATTTTCCAGTGTGTTAGTGTAAATAACATGTCAATTCGTGTAAACACTTCTTCG	2940
Db	2881	ATGATGATTTTCCAGTGTGTTAGTGTAAATAACATGTCAATTCGTGTAAACACTTCTTCG	2940
Qy	2941	TTCCGCAAAATCCTCAGTTGAAATTTTAAATTTTCCACGCGCAGTAAAAAATAA	2991
Db	2941	TTCCGCAAAATCCTCAGTTGAAATTTTAAATTTTCCACGCGCAGTAAAAAATAA	2991

Search completed: June 4, 2004, 22:21:11

OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 21:05:07 ; Search time 7571.55 Seconds  
(without alignments)  
11796.502 Million cell updates/sec

Title: US-10-671-628-3  
Perfect score: 2991  
Sequence: 1 tgggtgtgacgagtgacgag.....ccagccagtaaaaaaaaaa 2991

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues  
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*

28: gb\_gss1:\*  
29: gb\_gss2:\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.  
SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length	†			
1	400.4	13.4	762	14	CF213174	CF213174	CGP100063
2	381	12.7	871	14	CB250646	CB250646	UCRCS010
3	365.2	12.2	1241	14	CB330501	CB330501	SPEST485
4	363.2	12.1	682	14	CF436214	CF436214	EST672559
5	363.2	12.1	719	14	CF445646	CF445646	EST681991
6	363.2	12.1	779	14	CF448435	CF448435	EST684780
7	361.2	12.1	712	14	CF452690	CF452690	EST689035
8	361	12.1	733	13	BQ972958	BQ972958	QHL116222
9	360	12.0	649	14	CF442797	CF442797	EST679142
10	332.6	11.1	872	12	BG446588	BG446588	GA_Eb003
11	332	11.1	747	14	CD841700	CD841700	RF02.124F
12	330.4	11.0	679	12	BG450507	BG450507	RF019607D
13	325.6	10.9	769	14	CD829664	CD829664	BN40.042N
14	314.2	10.5	716	14	CD820766	CD820766	BN20.053M
15	311.6	10.4	709	13	BQ842169	BQ842169	WHE2989_F
16	311.6	10.4	766	13	BQ483475	BQ483475	WHE3509_A
17	310.8	10.4	816	14	CD818539	CD818539	BN20.045M
18	310	10.4	700	14	CD894584	CD894584	G118.126J
19	310	10.4	703	14	CD934959	CD934959	OV.002H09
20	307.4	10.3	768	12	BG321351	BG321351	DS01_07d1
21	303.4	10.1	715	10	BE454099	BE454099	HVSMER008
22	300.8	10.1	569	12	BN093699	BN093699	saj13b05.
23	299	10.0	706	13	BQ802519	BQ802519	WHE2826_H
24	295.8	9.9	994	12	BG416382	BG416382	HVSMER001
25	295.6	9.9	746	14	CD826833	CD826833	BN25.065D
26	293	9.8	610	13	BQ967986	BQ967986	QHB32H05.
27	292.8	9.8	742	12	BI979018	BI979018	zh02_Old
28	292	9.8	821	10	BE641808	BE641808	Cr12_4_F0
29	287.2	9.6	746	14	CF089986	CF089986	QHM3D13.y
30	285.4	9.5	736	14	CF133319	CF133319	WHE4356_E
31	280.6	9.4	481	12	BN360469	BN360469	GA_Ea003
32	279.4	9.3	897	10	BE055609	BE055609	GA_Ea003
33	276.8	9.3	676	12	BI955063	BI955063	HVSMER002
34	276	9.2	711	12	BG366223	BG366223	HVSMER1000
35	276	9.2	793	10	BE627613	BE627613	HVSMER000
36	275.8	9.2	757	13	BU010688	BU010688	GGJ14C11.
37	275.8	9.2	1447	13	BU103700	BU103700	SCEPAM201
38	275.4	9.2	639	14	CD825105	CD825105	BN25.059L
39	273.8	9.2	535	12	BM520694	BM520694	sak97d07.
40	273.2	9.1	1422	11	AY105357	AY105357	Zea_mays
41	273	9.1	470	9	AI162254	AI162254	A014P69U
42	272.6	9.1	797	13	BQ743348	BQ743348	WHE4102_H
43	272.2	9.1	647	13	BU997283	BU997283	HI07H02r
44	270.2	9.0	642	10	BE601596	BE601596	HVSMER009
45	269.4	9.0	650	13	CA015462	CA015462	HT14G05r

Search completed: June 5, 2004, 06:21:15  
Job time : 7575.55 secs